



## SEQUENCE LISTING

<110> Structural GenomiX, Inc.  
Atwell, Shane  
Buchanan, Sean G.

<120> Crystals and Structures of Epidermal Growth Factor Receptor Kinase Domain

<130> 022132-000910US

<140> 10/801,266

<141> 2004-03-16

<150> US 60/456,553

<151> 2003-03-20

<160> 8

<170> PatentIn version 3.1

<210> 1

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<212> DNA

<213> Artificial Sequence

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<223> forward primer

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gctccaacc aagctctc

18

<210> 2

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<223> reverse primer

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20

<210> 3  
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<212> DNA  
<213> Artificial Sequence

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<223> sequence after being ligated into vector

<400> 3  
aaggcatca tcaccatcac cactga 26

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<211> 297  
<212> PRT  
<213> Artificial Sequence

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<223> predicted sequence of EGFRKD expressed protein

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Met Ala Leu Ala Pro Asn Gln Ala Leu Leu Arg Ile Leu Lys Glu Thr  
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Glu Phe Lys Lys Ile Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val  
20 25 30

Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu Lys Val Lys Ile Pro Val  
35 40 45

Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser Pro Lys Ala Asn Lys Glu  
50 55 60

Ile Leu Asp Glu Ala Tyr Val Met Ala Ser Val Asp Asn Pro His Val  
65 70 75 80

Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Ile Thr  
85 90 95

Gln Leu Met Pro Phe Gly Cys Leu Leu Asp Tyr Val Arg Glu His Lys  
100 105 110

Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn Trp Cys Val Gln Ile Ala  
115 120 125

Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg Leu Val His Arg Asp Leu  
130 135 140

Ala Ala Arg Asn Val Leu Val Lys Thr Pro Gln His Val Lys Ile Thr  
145 150 155 160

Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala Glu Glu Lys Glu Tyr His  
165 170 175

Ala Glu Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile  
180 185 190

Leu His Arg Ile Tyr Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val  
195 200 205

Thr Val Trp Glu Leu Met Thr Phe Gly Ser Lys Pro Tyr Asp Gly Ile  
210 215 220

Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu Lys Gly Glu Arg Leu Pro  
225 230 235 240

Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys  
245 250 255

Trp Met Ile Asp Ala Asp Ser Arg Pro Lys Phe Arg Glu Leu Ile Ile  
260 265 270

Glu Phe Ser Lys Met Ala Arg Asp Pro Gln Arg Tyr Leu Val Ile Gln  
275 280 285

Gly Glu Gly His His His His His His  
290 295

<210> 5

<211> 290

<212> PRT

<213> Homo sapiens

<400> 5

Met Ala Leu Ala Pro Asn Gln Ala Leu Leu Arg Ile Leu Lys Glu Thr  
1 5 10 15

Glu Phe Lys Lys Ile Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val

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 Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu Lys Val Lys Ile Pro Val  
     35                      40                      45  
 Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser Pro Lys Ala Asn Lys Glu  
     50                      55                      60  
 Ile Leu Asp Glu Ala Tyr Val Met Ala Ser Val Asp Asn Pro His Val  
     65                      70                      75                      80  
 Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Ile Thr  
             85                      90                      95  
 Gln Leu Met Pro Phe Gly Cys Leu Leu Asp Tyr Val Arg Glu His Lys  
             100                      105                      110  
 Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn Trp Cys Val Gln Ile Ala  
             115                      120                      125  
 Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg Leu Val His Arg Asp Leu  
             130                      135                      140  
 Ala Ala Arg Asn Val Leu Val Lys Thr Pro Gln His Val Lys Ile Thr  
     145                      150                      155                      160  
 Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala Glu Glu Lys Glu Tyr His  
             165                      170                      175  
 Ala Glu Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile  
             180                      185                      190  
 Leu His Arg Ile Tyr Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val  
             195                      200                      205  
 Thr Val Trp Glu Leu Met Thr Phe Gly Ser Lys Pro Tyr Asp Gly Ile  
             210                      215                      220  
 Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu Lys Gly Glu Arg Leu Pro  
     225                      230                      235                      240  
 Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys  
             245                      250                      255  
 Trp Met Ile Asp Ala Asp Ser Arg Pro Lys Phe Arg Glu Leu Ile Ile  
             260                      265                      270

Glu Phe Ser Lys Met Ala Arg Asp Pro Gln Arg Tyr Leu Val Ile Gln  
275 280 285

Gly Glu  
290

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<212> PRT  
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<223> HER2/ErbB2

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Ser Gly Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr  
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Glu Leu Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val  
20 25 30

Tyr Lys Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val  
35 40 45

Ala Ile Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu  
50 55 60

Ile Leu Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val  
65 70 75 80

Ser Arg Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr  
85 90 95

Gln Leu Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg  
100 105 110

Gly Arg Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala  
115 120 125

Lys Gly Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu  
130 135 140

Ala Ala Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr

145            150            155            160  
 Asp Phe Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His  
           165            170            175  
 Ala Asp Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile  
           180            185            190  
 Leu Arg Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val  
           195            200            205  
 Thr Val Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile  
           210            215            220  
 Pro Ala Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro  
 225            230            235            240  
 Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys  
           245            250            255  
 Trp Met Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser  
           260            265            270  
 Glu Phe Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln  
           275            280            285  
 Asn

<210> 7  
 <211> 290  
 <212> PRT  
 <213> Unknown

<220>  
 <223> HER4/ErbB4

<400> 7

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Glu Leu Lys Arg Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val  
           20            25            30

Tyr Lys Gly Ile Trp Val Pro Glu Gly Glu Thr Val Lys Ile Pro Val  
35 40 45

Ala Ile Lys Ile Leu Asn Glu Thr Thr Gly Pro Lys Ala Asn Val Glu  
50 55 60

Phe Met Asp Glu Ala Leu Ile Met Ala Ser Met Asp His Pro His Leu  
65 70 75 80

Val Arg Leu Leu Gly Val Cys Leu Ser Pro Thr Ile Gln Leu Val Thr  
85 90 95

Gln Leu Met Pro His Gly Cys Leu Leu Glu Tyr Val His Glu His Lys  
100 105 110

Asp Asn Ile Gly Ser Gln Leu Leu Leu Asn Trp Cys Val Gln Ile Ala  
115 120 125

Lys Gly Met Met Tyr Leu Glu Glu Arg Arg Leu Val His Arg Asp Leu  
130 135 140

Ala Ala Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr  
145 150 155 160

Asp Phe Gly Leu Ala Arg Leu Leu Glu Gly Asp Glu Lys Glu Tyr Asn  
165 170 175

Ala Asp Gly Gly Lys Met Pro Ile Lys Trp Met Ala Leu Glu Cys Ile  
180 185 190

His Tyr Arg Lys Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val  
195 200 205

Thr Ile Trp Glu Leu Met Thr Phe Gly Gly Lys Pro Tyr Asp Gly Ile  
210 215 220

Pro Thr Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro  
225 230 235 240

Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr Met Val Met Val Lys Cys  
245 250 255

Trp Met Ile Asp Ala Asp Ser Arg Pro Lys Phe Lys Glu Leu Ala Ala  
260 265 270

Glu Phe Ser Arg Met Ala Arg Asp Pro Gln Arg Tyr Leu Val Ile Gln

275	280	285
Gly Asp		
290		
<210> 8		
<211> 289		
<212> PRT		
<213> Unknown		
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Ser Glu Lys Ala Asn Lys Val Leu Ala Arg Ile Phe Lys Glu Thr Glu		
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Leu Arg Lys Leu Lys Val Leu Gly Ser Gly Val Phe Gly Thr Val His		
20	25	30
Lys Gly Val Trp Ile Pro Glu Gly Glu Ser Ile Lys Ile Pro Val Cys		
35	40	45
Ile Lys Val Ile Glu Asp Lys Ser Gly Arg Gln Ser Phe Gln Ala Val		
50	55	60
Thr Asp His Met Leu Ala Ile Gly Ser Leu Asp His Ala His Ile Val		
65	70	75 80
Arg Leu Leu Gly Leu Cys Pro Gly Ser Ser Leu Gln Leu Val Thr Gln		
85	90	95
Tyr Leu Pro Leu Gly Ser Leu Leu Asp His Val Arg Gln His Arg Gly		
100	105	110
Ala Leu Gly Pro Gln Leu Leu Leu Asn Trp Gly Val Gln Ile Ala Lys		
115	120	125
Gly Met Tyr Tyr Leu Glu Glu His Gly Met Val His Arg Asn Leu Ala		
130	135	140
Ala Arg Asn Val Leu Leu Lys Ser Pro Ser Gln Val Gln Val Ala Asp		
145	150	155 160



Phe Gly Val Ala Asp Leu Leu Pro Pro Asp Asp Lys Gln Leu Leu Tyr  
165 170 175

Ser Glu Ala Lys Thr Pro Ile Lys Trp Met Ala Leu Glu Ser Ile His  
180 185 190

Phe Gly Lys Tyr Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr  
195 200 205

Val Trp Glu Leu Met Thr Phe Gly Ala Glu Pro Tyr Ala Gly Leu Arg  
210 215 220

Leu Ala Glu Val Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Ala Gln  
225 230 235 240

Pro Gln Ile Cys Thr Ile Asp Val Tyr Met Val Met Val Lys Cys Trp  
245 250 255

Met Ile Asp Glu Asn Ile Arg Pro Thr Phe Lys Glu Leu Ala Asn Glu  
260 265 270

Phe Thr Arg Met Ala Arg Asp Pro Pro Arg Tyr Leu Val Ile Lys Arg  
275 280 285

Glu

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